

ATATTGCTGAGCTCAGGGAGTCAGGGCCCCACATTGAGACAGTCAAGCCCCAAGAAGAGG	60
GATCCCTGCTCCAGCAGCTGCAAGGTGCAAGAAGAAGAAGATCCCAGGAGGAAAAATGTG	120
CTGGAGACCCCTGTGTCGGTTCTCTGTGGTTTGGTCTATCTGTCTTATGTTCAACAGT	180
W R P L C R F I W L N S Y I S Y V O A V	22
GCCTATCCAGAAAGTCGAGGTACACCAAAACCTCATCAAGACCATTTGTCACCCAGGT	240
P I Q K A V Q G D D T K T L I K T I V T R I	42
CAATGCATTTTACACACCGCAGTCGGTATCCGCCAAGCAGAGGGTCACTGGCTGGACTT	300
N D I S H T Q S V S A K Q R V T G L D F	62
CATTCTGGGCTTCAACCCATTCTGAGTTTGTCCAAGATGGACCAAGTCTGGCAGTCTA	360
I P G L H P I L S L S K M D O T L A V	82
TCAACAGGTCTCTCACCAGCCTGCCCTTCCAAAAATGTGCTGCAGATAGCCAATGACCTGGA	420
Q Q V L T S L P S Q N V L Q I A N D L E	102
GAATCTCCGAGACCTCTCTCCATCTGCTGGCTTCTCCAAGAGCTGCTCCCTGCTCAGAC	480
N L A D L L H L L A T F S K S C S L P Q T	122
CAGTGGCTGCAGAAGCCACAGACCTGGATGGCTTCTCGAAGCCTCACTCTACTCCAC	540
S G C L Q K P E S L D G V L E A S L Y S T	142
AGAGGTGGTGGCTTTGAGCAGGCTGCAGGGCTCTCTGCAGGACATCTTCAACAGTTGGA	600
E V V A L S R L Q G S L Q D I L Q Q L D	162
TGTTAGCCCTGAATGCTGAAGTTTCAAAGGCCACCAAGGCTCCCAAGAATCATGTAGAGG	660
V S P E *	167
AAGAAACCTTGGCTTCCAGGGGTCTTCAGGAGAAGAGGCCATGTGCACACATCCATCAT	720
TCATTCTCTCCCTCCTGTAGACCACCCATCCAAAGGCATGACTCCACAATGCTTGACTC	780
AAGTTATCCACACAACCTTCATGAGCACAAAGGAGGGGCCAGCTGCAGAGGGGACTCTCAC	840
CTAGTTCTTCAGCAAGTAGAGATAAGAGCCATCCCATCCCCCATGTCCCACCTGCTCC	900
GGGTACATGTTCTCCGTGGGTACACGCTTCGCTGCGGCCCAAGGAGAGGTGAGGTAGGGA	960
TGGGTAGAGCCTTTGGGCTGTCTCAGAGTCTTTGGGAGCACCGTGAAGGCTGCATCCACA	1020
CACAGCTGGAACCTCCCAAGCAGCACAGATGGAAGCACTTATTTATTTATCTGCATTC	1080
TATTTTGGATGGATCTGAAGCAAGGCATCAGCTTTTTCAGGCTTTGGGGGTGAGCCAGGA	1140
TGAGGAAGGCTCTCGGGTGCTGCTTCAATCCTATTGATGGGTGCCCCGAGGCAAAAC	1200
TAATTTTGTAGTGACTGGAAGGAAGGTTGGGATCTTCCAAACAAGAGTCTATGCAGGTAG	1260
CGCTCAAGATTGACCTCTGGTGACTGGTTTTGTTTCTATTGTGACTGACTCTATCCAAAC	1320
ACGTTTGCAGCGGCATTGCCCGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTT	1380
TGTCAGGTGAATATGTATCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGT	1440
GAAGCATCCGGAAGTGTTCTCTGAAATTACATATGTGTGGTAGGCTTTTCTGAAAGGGTG	1500
GGCATTTTCTTACCTCTGTGGCCACATAGTGTGGCTTTGTGAAAAGGACAAAGGAGTTGA	1560
CTCTTTCCGGAACATTTGGAAGTACAGGACACCGCTTGGAGGGGCTAAGACTACAGCCCT	1620
TTTGTGGCATATTGCTGAGCTCAGGGAGTCCGGGCCCCACATTTGAGACAGTGAAGCCCC	1680
AAGAAAAGGGTCCCTGGTGATGATCTCCAAGGTTGCTCCAGGTTGATCTCACATGCGGTT	1740
TCTTAAGCAGGTAGACGTTTGCATGCCAATATGTGGTTCTCATCTGATTGGTTTATCCAA	1800
AGTAGAACCTGTCTCCCAACCATTTCTGTGGGAGGTTTGTGTTCCAGTGGGAATGAGAAAT	1860
CACCTAGCAGATGGTCTGAGCCCTGGGCCAGCACTGCTGAGGAAGTGCCAGGGGCCCCAG	1920
GCCAGGCTGCCAGAAATGCCCTTGGGGCTGGAGGATGAACAAAGGGGCTTGGGTTTTTC	1980
ATCACCCCTGCACCTATGTACCATCAAACTGGGGGGCAGATCAGTGAGAGGCACTTG	2040
ATGGAAGCAATACACTTTAAGACTGAGCACAGTTTCGTGCTCAGCTCTGTCTGTGGCTG	2100
TGAGCTAGAGAAGCTCACCACATACATATAAAATCAGAGGCTCATGTCCCTGTGGTTAG	2160
ACCTTACTCGGGGGGTGTACTCCACCACAGCAGCAGCCGACCGCTGGAAGTACAGTGCT	2220
GTCTTCAACAGGTGTGAAAGAACTGAGCTGAGGGTGACAGTGCCCAAGGGGAACCTGTCT	2280
TGCAGTCTATTGCATTTACATACCGCATTTACAGGGCATTAGCATCCACTCCTATGGTA	2340
GCACACTGTTGACAAATAGGACAAAGGATAGGGGTTGACTATCCCTTATCCAAAAATGCTTG	2400
GGACTAGAAGAGTTTTGGATTTTAGACTCTTTTCAGGCATAGGTATATTGAGTATATAT	2460
AAAATGAGATATCTTGGGGATGGGGCCCCAAGTATAAACATGAAGTTCATTTATTTTCAT	2520
AATACCGTATAGACACTGCTTGAAGTGATGTTTATACAGTGTTTTAAATAACGTTGTAT	2580
GCATGAAAGACGTTTTTACAGCATGAACCTGTCTACTCATGCCAGCACTCAAAAACCTTG	2640
GGGTTTTTGAGCAGTTTGGATCTTGGGTTTTCTGTGTTAAGAGATGGTTAGCTTATACCTAA	2700
AACCATAATGCAACAGGCTGCAGGACAGACGGATCCTCAGCCCTGAAGTGTGCCCT	2760
TCCAGCCAGGCTACATCCCTGTGGAGTGAGGGATCAGGTTTGTGGTGCTAAGAGAGG	2820
AGTTGAGGCTAGATTTTGGAGGATCTCAGGGC	2852

# Figure 2

---G--GTTG CAAGGCCCAA GAAGCCCA-- -TCCTGGGAA GGAAAATGCA	50
TTGGGGAACC CTGTG-CGGA TTCTTGTGGC TTTGGCCCTA TCTTTTCTAT	100
GTCCAAGCTG TGCCCATCCA AAAAGTCCAA GATGACACCA AAACCCTCAT	150
CAAGACAATT GTCACCAGGA TCAATGACAT TTCACACACG CAGTCAGTCT	200
CCTCCAAACA GAAAGTCACC GGT TTGGACT TCATTCTGG GCTCCACCCC	250
ATCCTGACCT TATCCAAGAT GGACCAGACA CTGGCAGTCT ACCAACAGAT	300
CCTCACCAGT ATGCCTTCCA GAAACGTGAT CCAAATATCC AACGACCTGG	350
AGAACCTCCG GGATCTTCTT CACGTGCTGG CCTTCTCTAA GAGCTGCCAC	400
TTGCCCTGGG CCAGTGGCCT GGAGACCTTG GACAGCCTGG GGGGTGTCCT	450
GGAAGCTTCA GGCTACTCCA CAGAGGTGGT GGCCCTGAGC AGGCTGCAGG	500
GGTCTCTGCA GGACATGCTG TGGCAGCTGG ACCTCAGCCC TGGGTGCTGA	550
GGCCTTGAAG GTCACTCTTC CTGCAAGGAC T-ACGTTAAG GGAAGGAACT	600
CTGGTTTCCA GGTATCTCCA GGATTGAAGA GCATTGCATG GACACCCCTT	650
ATCCAGGACT CTGTCAATTT CCCTGACTCC TCTAAGCCAC TCTTCCAAAG	700
G	701

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### Figure 3

1	Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr
16	Leu Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp
31	Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile
46	Ser His Thr Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu
61	Asp Phe Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met
76	Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro
91	Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg
106	Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys His Leu Pro
121	Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly Val Leu
136	Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu
151	Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro
166	Gly Cys End

## Figure 4

Mouse	MCWRPLCRFL	WLWSYLSYVQ	AVPIQKVQDD	TKTLIKTIVT	RINDISHTQS	50
	* * *	* *				
Human	MHWGTLGFL	WLWPYLFYVQ	AVPIQKVQDD	TKTLIKTIVT	RINDISHTQS	
Mouse	VSAKQRTGL	DFIPGLHPIL	SLSKMDQTLA	VYQQVLTSLP	SQNVLQIAND	100
	*		-	-	* *	
Human	VSSKQKVTGL	DFIPGLHPIL	TLKMDQTLA	VYQQILTSMP	SRNVIQISND	
Mouse	LENLRDLLHL	LAFSKSCSLP	QTSGLOKPPES	LDGVLEASLY	STEVVALSRL	150
	-	*	** ***-	* *		
Human	LENLRDLLHV	LAFSKSCHLP	WASGLETLDS	LGGVLEASGY	STEVVALSRL	
Mouse	QGSQDILQQ	LDVSPEC				167
	- *	- *				
Human	QGSQDMLWQ	LDLSPGC				

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## Figure 5

1 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr  
16 Leu Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp  
31 Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile  
46 Ser His Thr Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp  
61 Phe Ile Pro Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp  
76 Gln Thr Leu Ala Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser  
91 Gln Asn Val Leu Gln Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp  
106 Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys Ser Leu Pro Gln  
121 Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly Val Leu Glu  
136 Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln  
151 Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser Pro Glu  
166 Cys End

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1 Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr  
16 Leu Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp  
31 Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile  
46 Ser His Thr Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp  
61 Phe Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp  
76 Gln Thr Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser  
91 Arg Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp  
106 Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys His Leu Pro Trp  
121 Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly Val Leu Glu  
136 Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln  
151 Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro Gly  
166 Cys End

Figure 7

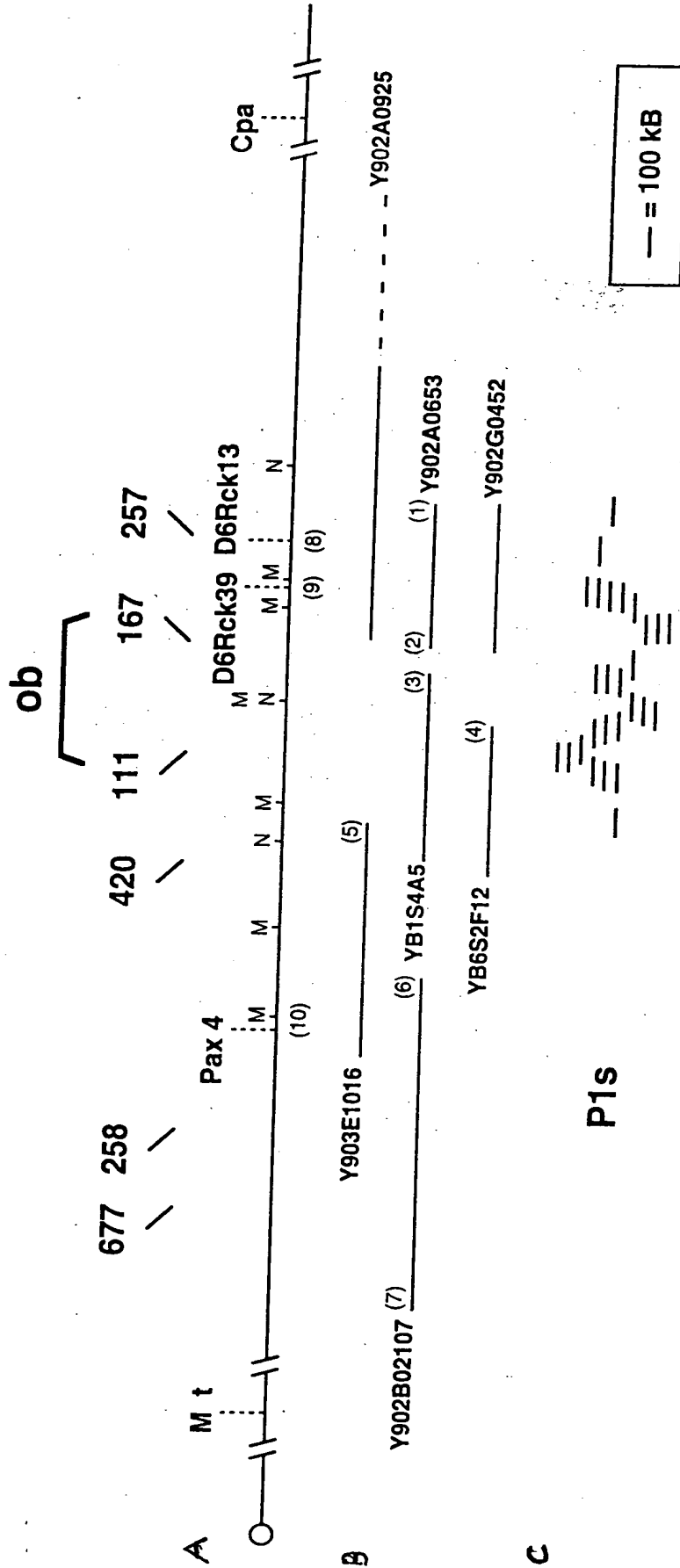
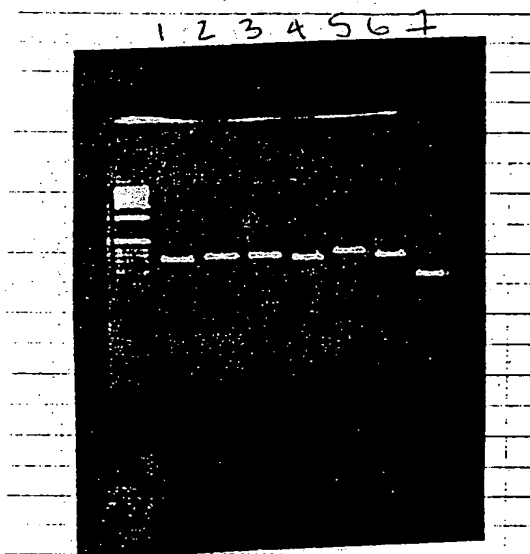




Figure 9



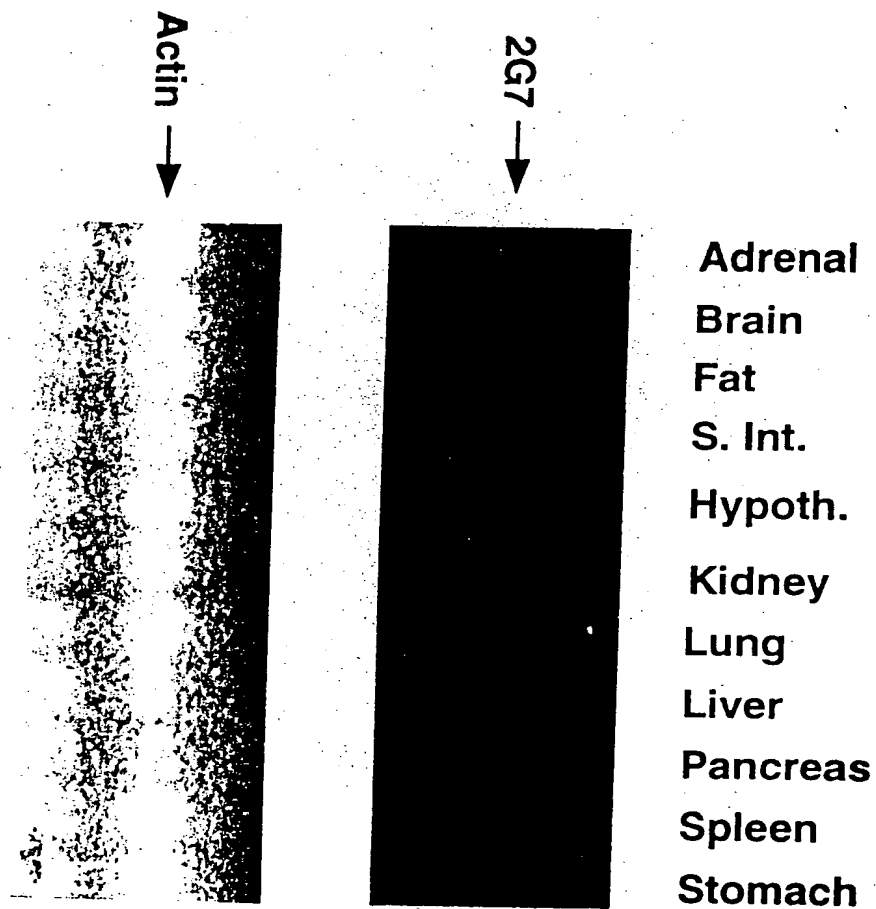
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Figure 10

+10 +20 +30 +40  
 1 GTGCAAGAAG AAGAAGATCC CAGGGCAGGA AAATGTCCTG GAGACCCCTG  
 CACGTTCTTC TTCTTCTAGG GTCCCGTCCT TTTACACGAC CTCTGGGGAC  
 +10 +20 +30 +40  
 51 TGTCGGGTCC NGTGGNTTTG GTCCTATCTG TCTTATGTNC AAGCAGTGCC  
 ACAGCCCAGG NCACCNAAC CAGGATAGAC AGAATACANG TTCGTCAAGG  
 +10 +20 +30 +40  
 101 TATCCAGAAA GTCCAGGATG ACACCAAAAG CCTCATCAAG ACCATTGTCA  
 ATAGGTCTTT CAGGTCCTAC TGTGGTTTTC GGAGTAGTTC TGGTAACAGT  
 +10 +20 +30 +40  
 NCAGGATCAC TGANATTTCA CACACG  
 151 ? ? ?  
 NGTCCTAGTG ACTNTAAAGT GTGTGC

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Figure 11A



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Figure 11B

18S —

28S —



white fat

brain

small intestine

stomach

pancreas

lung

testis

heart

spleen

liver

091626547 101000

Figure 12 B

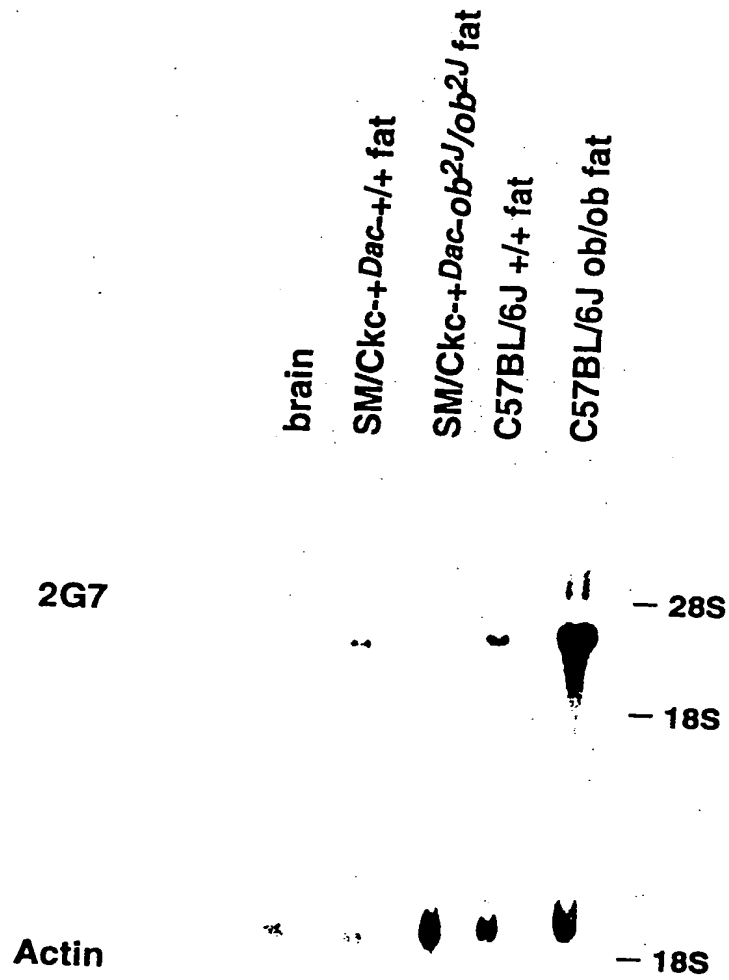
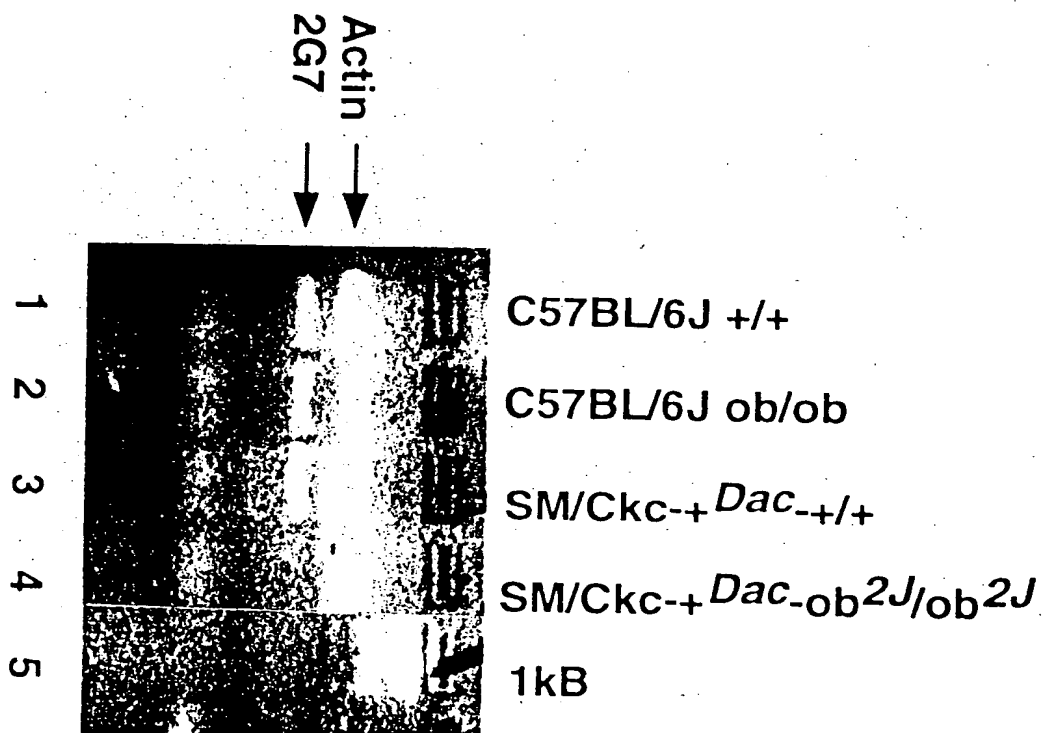
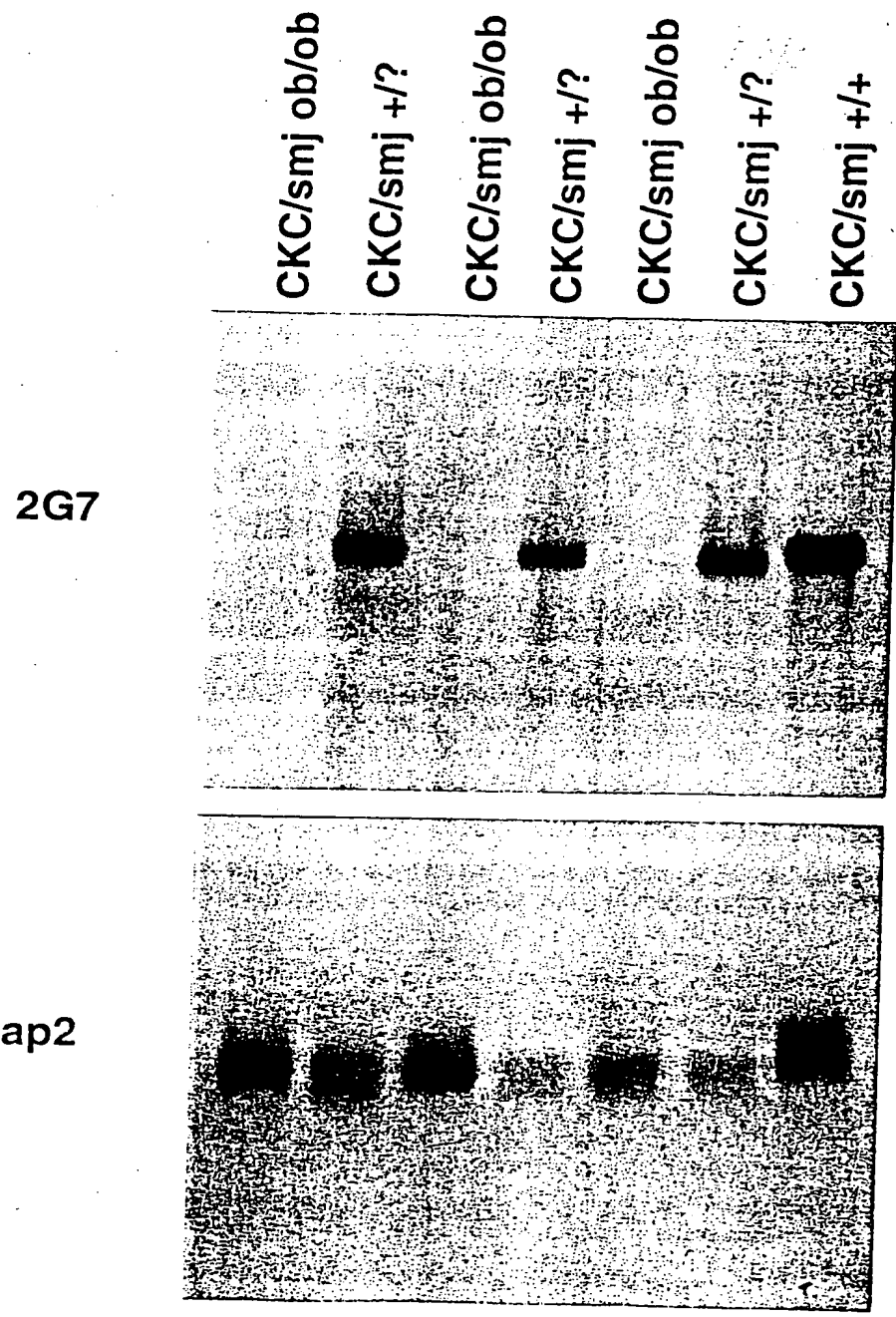


Figure 12A



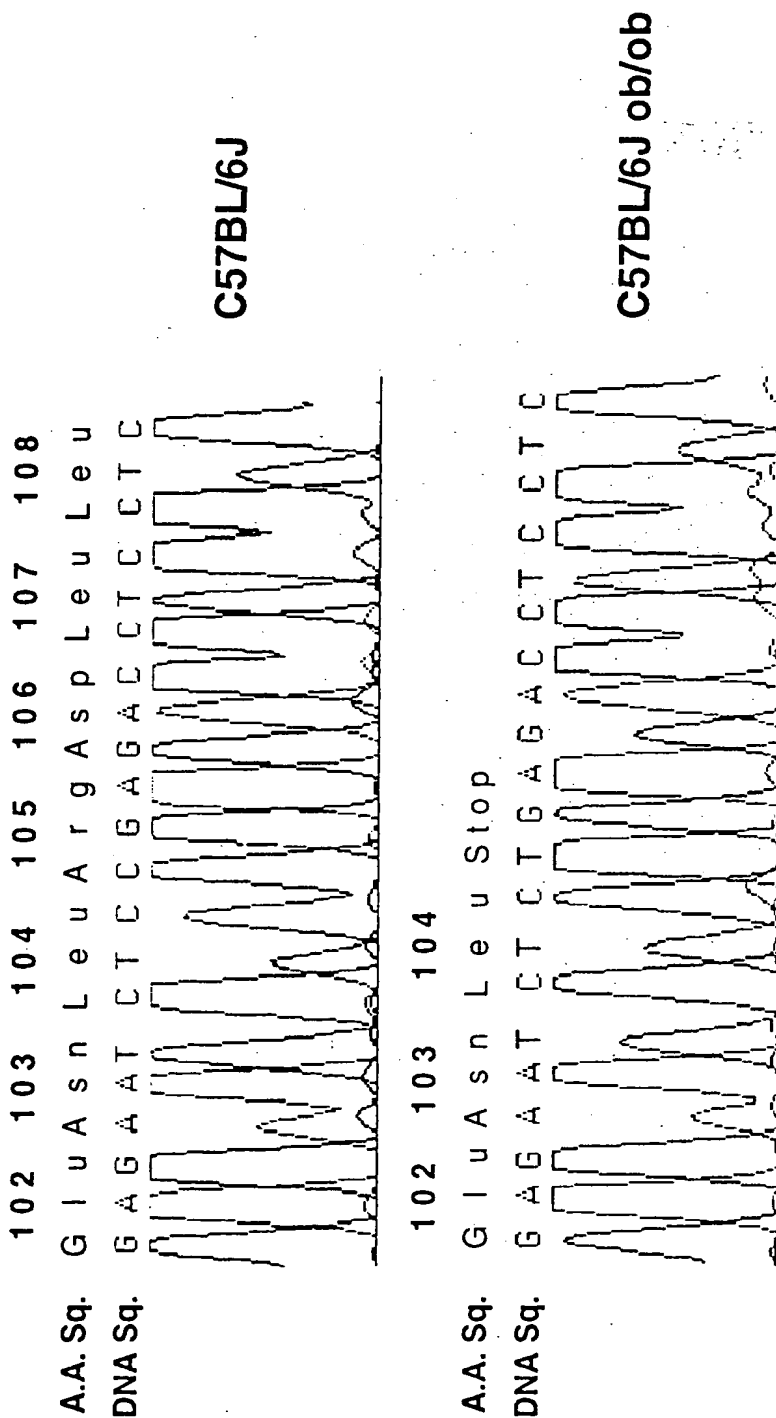
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Figure 13

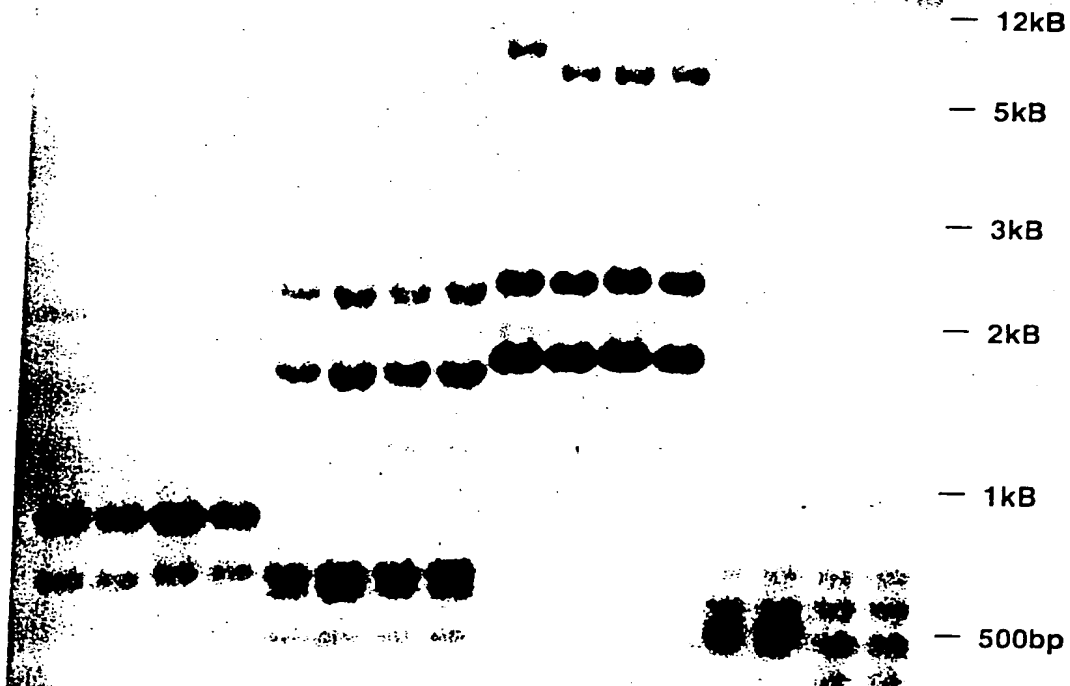


000000 4998960

Figure 14



Dpn II		Rsa I		Bgl II		Alu I	
SM/Ckc-+ <i>Dac</i> -ob2J/ob2J		SM/Ckc-+ <i>Dac</i> -ob2J/ob2J		SM/Ckc-+ <i>Dac</i> -ob2J/ob2J		SM/Ckc-+ <i>Dac</i> -ob2J/ob2J	
SM/Ckc-+ <i>Dac</i> .+/+		SM/Ckc-+ <i>Dac</i> .+/+		SM/Ckc-+ <i>Dac</i> .+/+		SM/Ckc-+ <i>Dac</i> .+/+	
C57BL/6J ob/ob		C57BL/6J ob/ob		C57BL/6J ob/ob		C57BL/6J ob/ob	
C57BL/6J +/+		C57BL/6J +/+		C57BL/6J +/+		C57BL/6J +/+	



**BglII Digests**

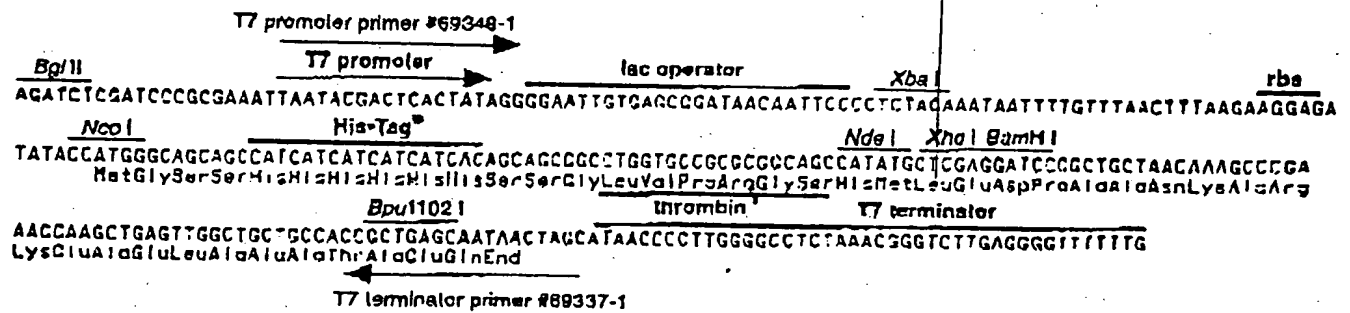
**+/+ control**

obese  
lean  
obese  
lean  
obese  
lean  
obese  
lean  
obese  
lean  
obese

The image shows a gel electrophoresis result for BglII digests. The lanes are labeled from left to right: +/+ control, obese, lean, obese, lean, obese, lean, obese, lean, obese, lean, obese. The control lane shows a single band. The obese lanes show multiple bands, indicating a mutation. The lean lanes show a single band, indicating no mutation.

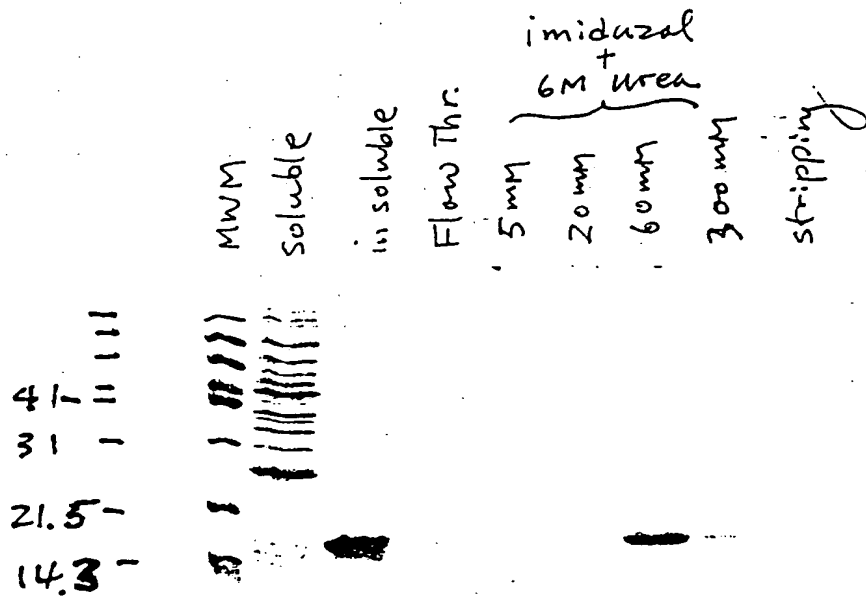


Figure 17



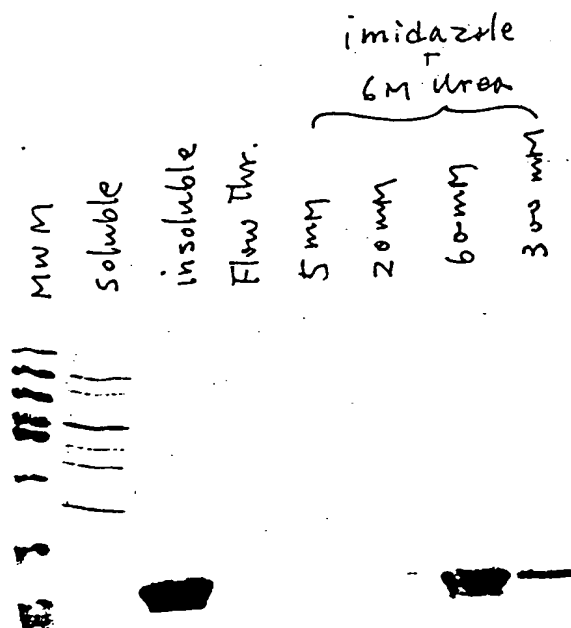
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Figure 18 A



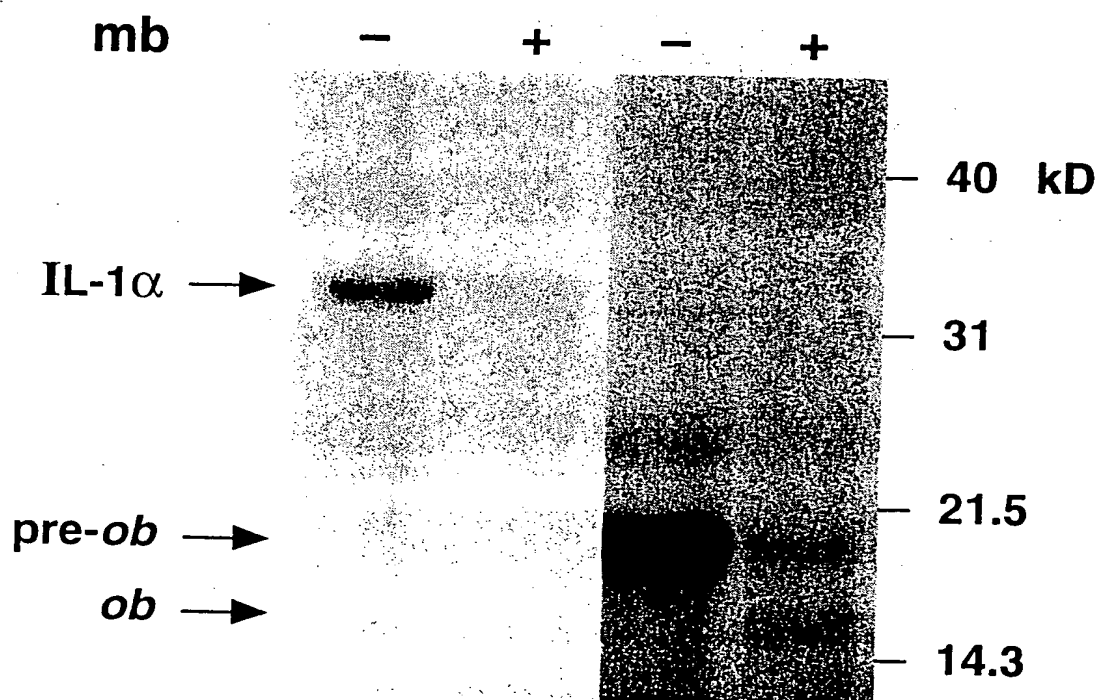
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Figure 18B



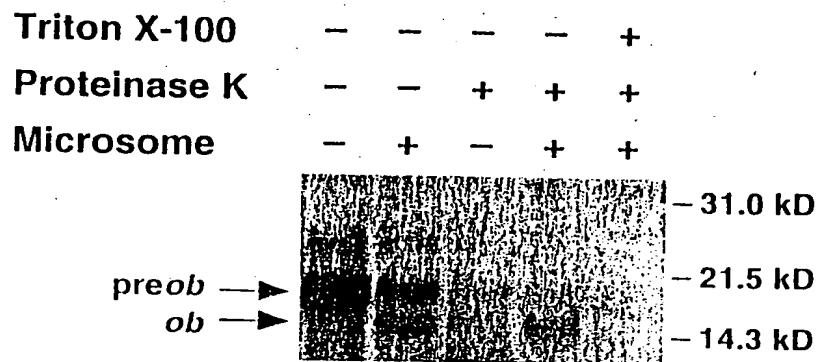
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Figure 19A



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Figure 19B



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Figure 20A

10	20	30	40	50
GGTTGCAAGG CCCAAGAAGC CCATCCTGGG AAGGAAAATG CATTGGGGAA				
60	70	80	90	100
CCCTGTGCGG ATTCTTGTGG CTTTGGCCCT ATCTTTTCTA TGTCCAAGCT				
110	120	130	140	150
GTGCCCATCC AAAAAGTCCA AGATGACACC AAAACCCTCA TCAAGACAAT				
160	170	180	190	200
TGTCAACAGG ATCAATGACA TTTCACACAC GGTAAAGGAGA GTATGCGGGG				
210	220	230	240	250
ACAAAGTAGA ACTGCAGCCA GCCCAGCACT GGCTCCTAGT GGCCTGGAC				
260	270	280	290	300
CCAGATAGTC CAAGAAACAT TTATTGAACG CCTCCTGAAT GCCAGGCACC				
310	320	330	340	350
TACTGCAAGC TGAGAAGGAT TTTGGATAGC ACAGGCCTCC ACTCTTCTG				
360	370	380	390	400
GTTGTTTCTT NTGGCCCCCT CTGCCTGCTG AGATNCCAGG GGTTAGNGGT				
410	420	430	440	450
TCTTAATTCC TAAA GAP OF SEQUENCE (~1.4 kb) CT				
460	470	480	490	500
GGTTCTTTCA GGAAGAGGCC ATGTAAGAGA AAGGAATTGA CCTAGGGAAA				
510	520	530	540	550
ATTGGCCTGG GAAGTGGAGG GAACGGATGG TGTGGGAAAA GCAGGAATCT				
560	570	580	590	600
CGGAGACCAG CTTAGAGGCT TGGCAGTCAC CTGGGTGCAG GANACAAGGG				
610	620	630	640	650
CCTGAGCCAA AGTGGTGAGG GAGGGTGGAA GGAGACAGCC CAGAGAATGA				
660	670	680	690	700
CCCTCCATGC CCACGGGGAA GGCAGAGGGC TCTGAGAGCG ATTCTCCCA				
710	720	730	740	750
CATGCTGAGC ACTTGTCTC CCTCTTCTC CTNCATAGCA GTCAGTCTCC				
760	770	780	790	800
TCCAAACAGA AAGTCACCGG TTTGGACTTC ATTCTGGGC TCCACCCCAT				
810	820	830	840	850
CCTGACCTTA TCCAAGATGG ACCAGACACT GGCAGTCTAC CAACAGATCC				
860	870	880	890	900
TCACCAGTAT GCCTTCCAGA AACGTGATCC AAATATCCAA CGACCTGGAG				

910	920	930	940	950
AACCTCCGGG ATCTTCTTCA CGTGCTGGCC TTCTCTAAGA GCTGCCACTT				
960	970	980	990	1000
GCCCTGGGcC AGTGGCCTGG AGACCTTGA CAGCCTGGG GGTGTCCTGG				
1010	1020	1030	1040	1050
AAGCTTCAGG CTACTCCACA GAGGTGGTGG CCCTGAGCAG GCTGCAGGGG				
1060	1070	1080	1090	1100
TCTCTGCAGG ACATGCTGTG GCAGCTGGAC CTCAGCCCTG GGTGCTGAGG				
1110	1120	1130	1140	1150
CCTTGAAGGT CACTCTTCTT GCAAGGACTA CGTTAAGGGA AGGAACCTCTG				
1160	1170	1180	1190	1200
GCTTCCAGGT ATCTCCAGGA TTGAAGAGCA TTGCATGGAC ACCCCTTATC				
1210	1220	1230	1240	1250
CAGGACTCTG TCAATTTCCT TGACTCCTCT AAGCCACTCT TCCAAAGG				

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Figure 20B

MOUSE OB STRUCTURE

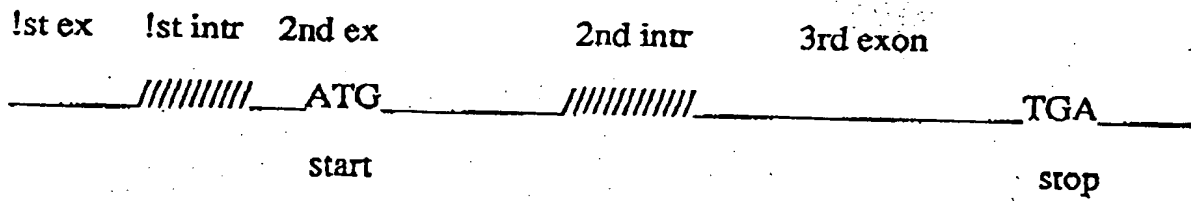
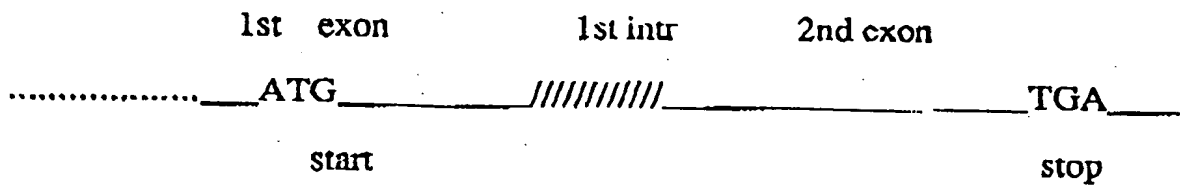


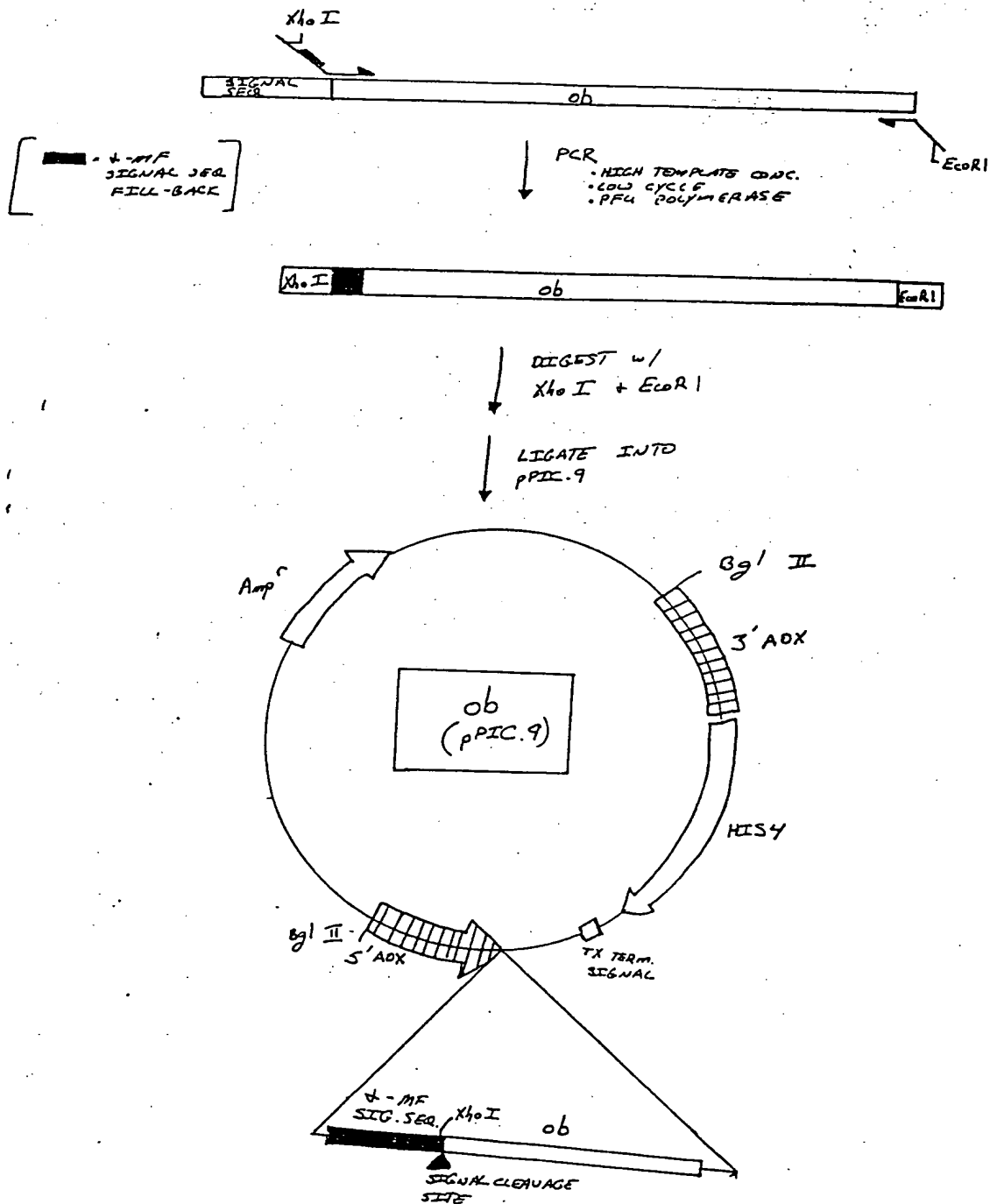
Figure 20c

HUMAN OB STRUCTURE



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Figure 21A



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Figure 21 B

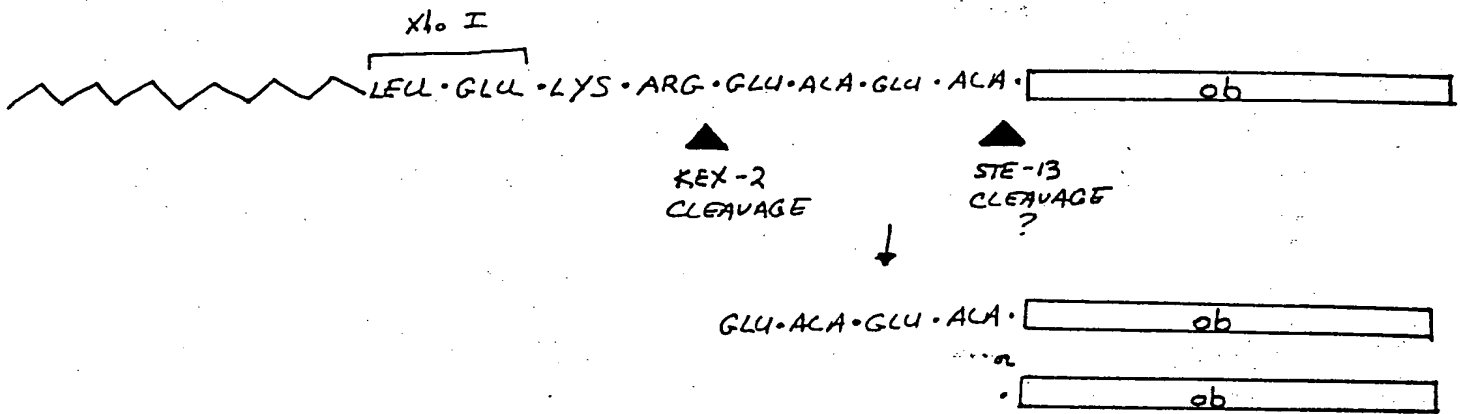
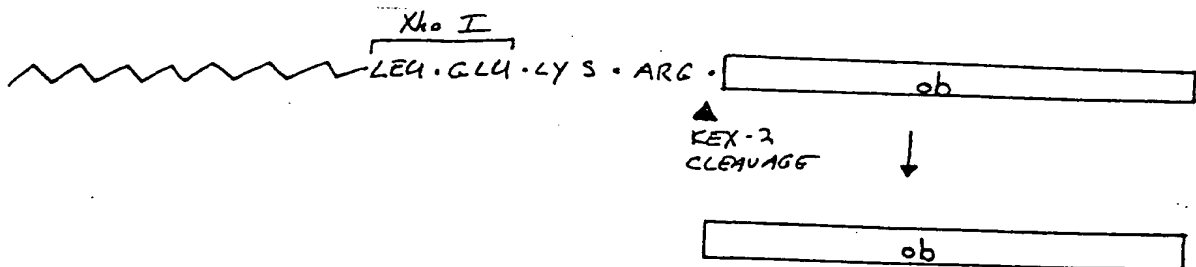
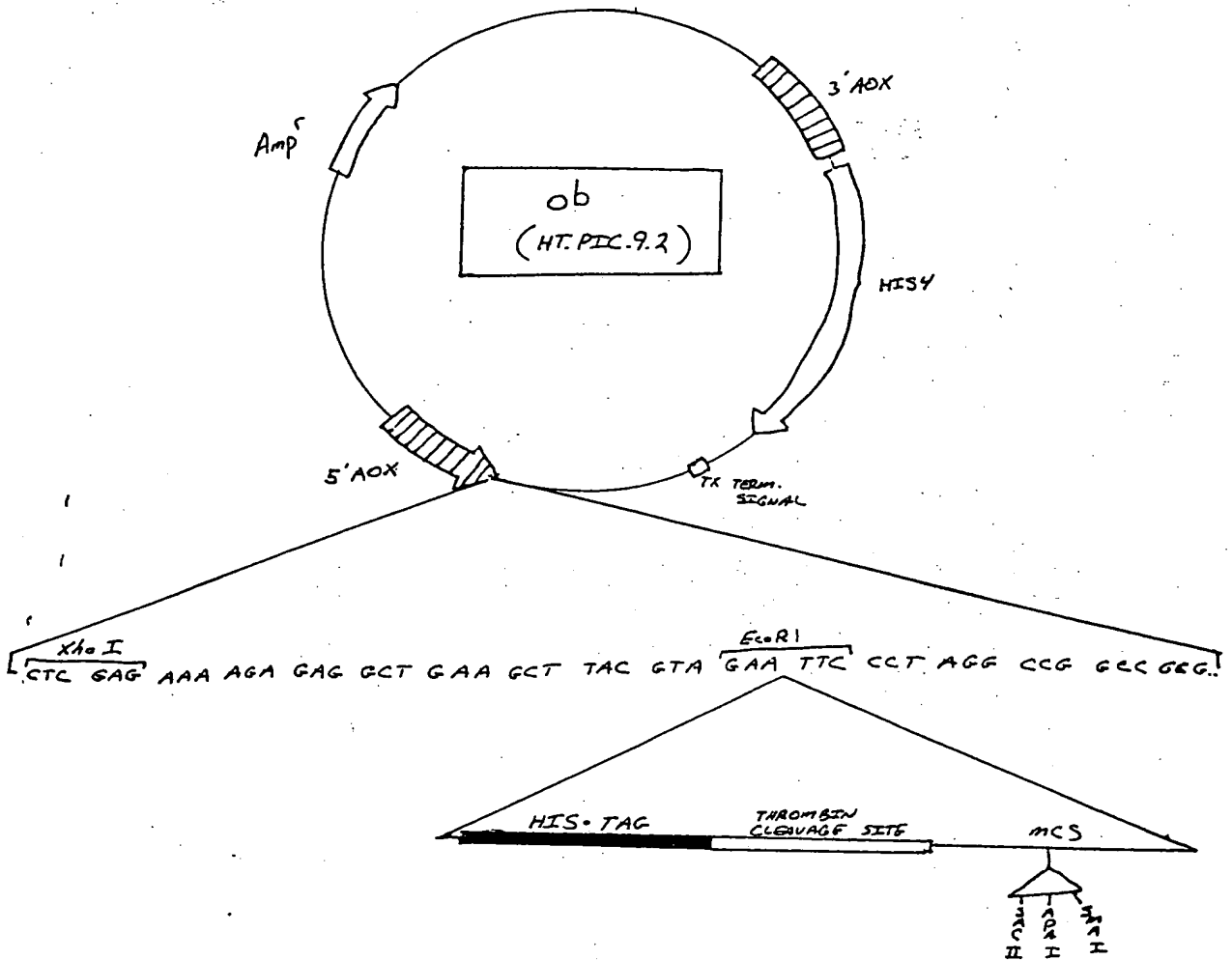


Figure 21 c



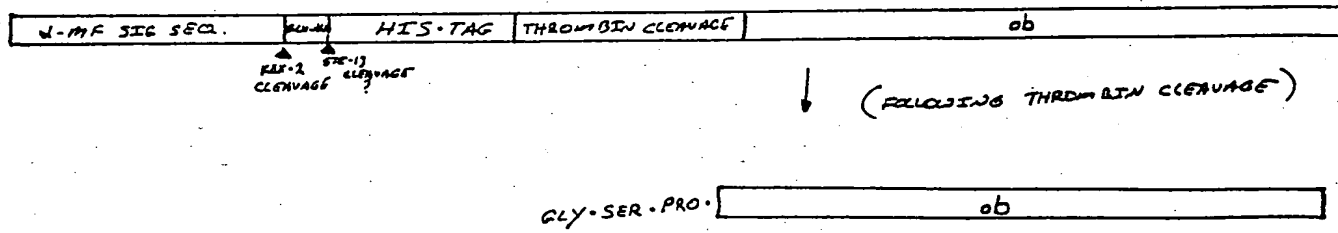
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Figure 22A



000001 2498860 09585647 101000

Figure 22B



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Figure 23A-

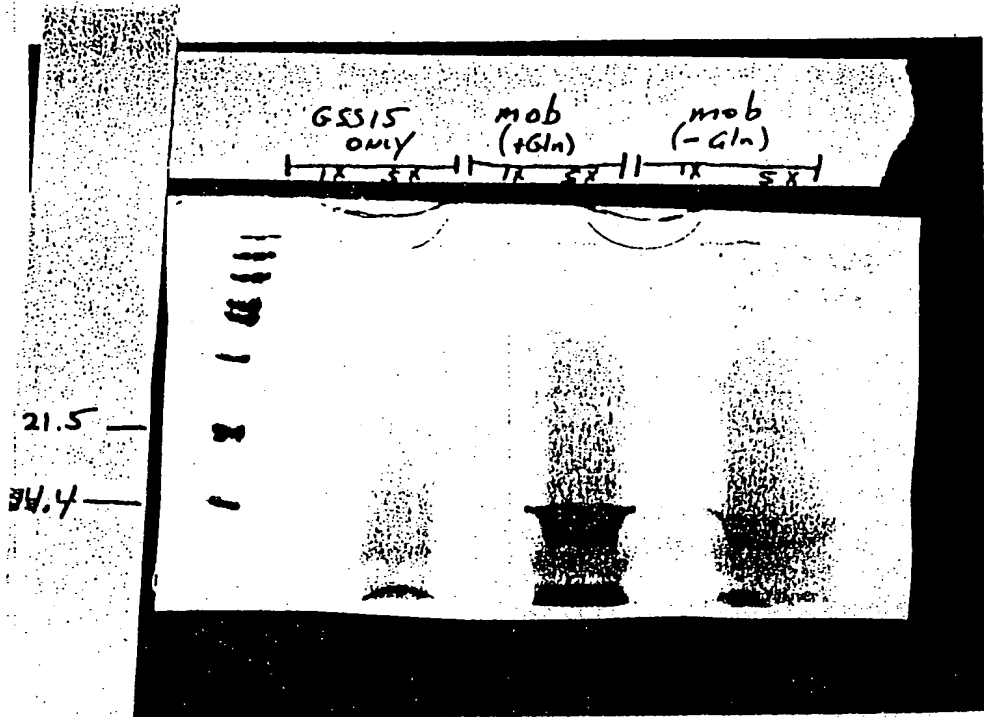
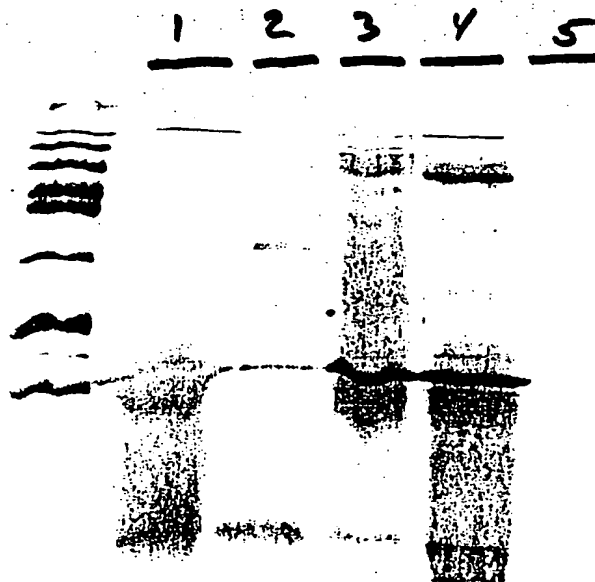


Figure 23B



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